

FIG. 1A

EcoRIa **24** **39** **54**
GAATTCGGG TGC AGG ACG AAG CTG TTC TGG ATT TCT TAC AGT GAT GGG GAC CAG
 Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln

69 **84** **99**
 TGT GCC TCA AGT CCA TGC CAG AAT GGG GGC TCC TGC AAG GAC CAG CTC CAG TCC
 Cys Ala Ser Ser Pro Cys Gln Asn Gly Ser Cys Lys Asp Gln Leu Gln Ser

114 **129** **144** **159**
 TAT ATC TGC TTC TGC CTC CCT GCC TTC GAG GGC CGG AAC, TGT GAG ACC CAC AAG
 Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys

174 **189** **204** **Pst Ia**
 GAT GAC CAG CTG ATC TGT GTG AAC GAG AAC GGC GGC TGT GAG CAG TAC TGC AGT
 Asp Asp Gln Leu Ile Cys Val Asn Glu Asp Gly Gly Cys Gln Tyr Cys Ser

219 **234** **249** **264**
 GAC CAC ACG GGC ACC AAG CGC TCC TGT CGG TGC CAC GAG GGG TAC TCT CTG CTG
 Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu

279 **294** **309** **324**
 GCA GAC GGG GTG TCC TGC ACA CCC ACA GTT GAA TAT CCA TGT GGA AAA ATA CCT
 Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro

Xba I **339** **354** **369**
ATT CTA GAA AAA AGA AAT GCC AGC AAA CCC CAA GGC CGA ATT GTG GGG GGC AAG
 Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys

384 **399** **414** **429**
 GTG TGC CCC AAA GGG GAG TGT CCA TGG CAG GTC CTG GTG TTG GTG AAT GGA GCT
 Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Leu Val Asn Gly Ala

444 **459** **474**
 CAG TTG TGT GGG GGG ACC CTG ATC AAC ACC ATC TGG GTG GTC TCC GCG GCC CAC
 Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His

489 **504** **519** **534**
 TGT TTC GAC AAA ATC AAG AAC AAC TGG AGG AAC CTG ATC GCG GTG CTG GCG GAG CAC
 Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His

549 **564** **579** **594**
 GAC CTC AGC GAG CAC GAC GGG GAT GAG CAG AGC CGG CGG GTG GCG CAG GTC ATC
 Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile

609 **Sma I** **624** **639**
 ATC CCC AGC ACG TAC GTC CCG GGC ACC ACC AAC CAC GAC ATC GCG CTG CTC CGC
 Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg

654 **669** **684** **699**
 CTG CAC CAG CCC GTG GTC CTC ACT GAC CAT GTG GTG CCC CTC TGC CTG CCC GAA
 Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu

714 729 744
 CGG ACG TTC TCT GAG AGG ACG CTG GCC TTC GTG CGC TTC TCA TTG GTC AGC GGC
 Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly

 759 774 Nar I 789 804
 TGG GGC CAG CTG CTG GAC CGT GGC GCC ACC GGC CTG GAG CTC ATG GTC CTC AAC
 Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Ieu Met Val Leu Asn

 819 834 Pst Ib 849 864
 GTG CCC CGG CTG ATG ACC CAG GAC TGC CTG CAG CAG TCA CGG AAG GTG GGA GAC
 Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp

 879 894 909
 TCC CCA AAT ATC ACG GAG TAC ATG TTC TGT GCC GGC TAC TCG GAT GGC AGC AAG
 Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys

 924 939 954 969
 GAC TCC TGC AAG GGG GAC AGT GGA GGC CCA CAT GCC ACC CAC TAC CGG GGC ACG
 Asp Ser Cys Lys Gly Asp Ser Gly Pro His Ala Thr His Tyr Arg Gly Thr

 984 999 1014
 TGG TAC CTG ACG GGC ATC GTC AGC TGG GGC CAG GGC TGC GCA ACC GTG GGC CAC
 Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His

 1029 1044 1059 TaqI 1074
 TTT GGG GTG TAC ACC AGG GTC TCC CAG TAC ATC GAG TGG CTG CAA AAG CTC ATG
 Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met

 1089 1104 1119 1138
 CGC TCA GAG CCA CGC CCA GGA GTC CTC CTG CGA GCC CCA TTT CCC TAG CCCAGCAGCC
 Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

 1148 1158 1168 1178 1188 1198 1208
CTGGCCTGTG GAGAGAAAGC CAAGGCTGCC TCGAAGTGT CTGGCACCAA ATCCCCATAA TTCTTCTGCA

 1218 1228 1238 1248 1258 1268 1278
GTTAATGGGG TAGAGGAGGG CATGGGAGGG AGGGAGAGGT GGGGAGGGAG ACAGAGACAG AAACAGAGAG

 1288 1298 1308 1318 1328 1338 1348
 AGACAGAGAC AGAGAGAGAC TGAGGGAGAG ACTCTGAGGA CCATGGAGAG AGACTCAAAG AGACTCCAAG

 1358 1368 1378 1388 1398 1408 1418
 ATTCAAAGAG ACTAATAGAG ACACAGAGAT GGAATAGAAA AGATGAGAGG CAGAGGCAGA CAGGGCCTGG

 1428 1438 1448 1458 1468 1478 1488
 ACAGAGGGGC AGGGGAGTGC CAAGGTTGTC CTGGAGGCCAG ACAGGCCAGC TGAGGCTCCT TACCTCCCTT

1498	1508	1518	1528	1538	1548	1558
CAGCCAAGCC	CCACCTGCAC	GTGATCTGCT	GGCCCTCAGG	CTGCTGCTCT	GCCTTCATTG	CTGGAGACAG
1568	1578	1588	1598	1608	1618	1628
TAGAGGCCATG	ACACACATGG	ATGCCACACAC	ACACACGCCA	TGCACACACA	CAGAGATATG	CACACACACG
1638	1648	1658	1668	1678	1688	1698
GATGCCACACA	CAGATGGTCA	CACAGACTAC	GCAAACACAC	CGATGCACAC	GCACATAGAG	ATATGCACAC
1708	1718	1728	1738	1748	1758	1768
ACAGATGCAC	ACACAGATAT	ACACATGGAG	TGCACGCACA	TGCCAATCCA	CGCACACATC	AGTGCACACG
1778	1788	1798	1808	1818	1828	1838
GATGCCACAGA	GATATGCACA	CACCGATGTG	CGCACACACA	GATATGCACA	CACATGGATG	ACACACACAC
1848	1858	1868	1878	1888	1898	1908
CACCAAGTGC	GCACACACAC	CGATGTACAC	ACAGATGCAC	ACACAGATGC	ACACACACCG	ATGCTGACTC
1918	1928	1938	1948	1958	1968	1978
CATGTTGCT	GTCCCTGTGAA	GGCGGTTGTT	TAGCTCTCAC	TTTTCTGGTT	CTTATCCATT	ATCATCTTCA
1988	1998	2008	2018	2028	2038	2048
CTTCAGACAA	TTCAGAGAGCA	TCACCATGCA	TGGTGGCGAA	TGCCCCAAA	CTCTCCCCA	AATGTATTTC
2058	2068	2078	2088	2098	2108	2118
TCCCCTTCGCT	GGGTGCCGGG	CTGCACAGAC	TATTCCCCAC	CTGCTTCCCA	GCTTCACAAT	AAACGGCTGC
2128	2138	2148	2158	2168	EcoRIB	
GTCTCTCGC	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAGGAATTC	

FIG. 1B

-60
Met Val Ser Gln Ala Leu Arg Leu Leu

TCAACAGGCAGGGCAGCACTGCAGAGATTTCATCATGGTCTCCCAGGCCCTCAGGCTCCTC
 10 20 30 40 50 60

-50 -40 ↓
Cys Leu Leu Leu Gly Leu Gln Gly Cys Leu Ala Ala Gly Gly Val Ala Lys Ala Ser Gly Gly
 TGCCTCTGCTTGGGCTTCAGGGCTGCTGGCTGCAGGCAGGGCTCGCTAAGGCCTCAGGAGGA
 70 80 90 100 110 120

-30 -20 ↓
Glu Thr Arg Asp Met Pro Trp Lys Pro Gly Pro His Arg Val Phe Val Thr Gln Glu Glu
 GAAACACGGGACATGCCGTGGAAGCCGGGGCTCACAGAGTCTTCGTAACCCAGGAGGA
 130 140 150 160 170 180

-10 -1 +1 +10
Ala His Gly Val Leu His Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
 GCCCACGGCGTCTGCACCGCGCCGCCAACCGCGTTCTGGAGGAGCTGCGGCCG
 190 200 210 220 230 240

+20 +30
Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile
 GGCTCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGAGGAGGCCGGAGATC
 250 260 270 280 290 300

+40 +50
Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys
 TTCAAGGACCGGGAGAGGACGAAGCTGTTCTGGATTCTACAGTGATGGGGACCAAGTG
 310 320 330 340 350 360

+60 +70
Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys
 GCCTCAAGTCATGCCAGAATGGGGCTCTGCACAGGACCAGCTCCAGTCCTATATCTGC
 370 380 390 400 410 420

+80 +90
Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
 TTCTGCCTCCCTGCCCTCGAGGGCGGAAGTGTGAGACGCACAAAGGATGACCAGCTGATC
 430 440 450 460 470 480

+100 +110
Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
 TGTGTGAACGAGAACGGCGCTGTGAGCAGTACTGCACTGACCAACGGGCACCAAGCGC
 490 500 510 520 530 540

+120 +130
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Ala Asp Gly Val Ser Cys Thr Pro Thr
 TCCTGTGGTGCACAGAGGGTACTCTGCTGGCAGACGGGGTGTCCCTGCACACCCACA
 550 560 570 580 590 600

+140 +150
Val Gln Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln
 GTTGAATATCCATGTGGAAAAATACCTATTCTAGAAAAAAAGAAATGCCAGCAAACCCCAA
 610 620 630 640 650 660

+160 +170
 Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Val Leu
 GCGGAAATTCTGGGGCAAGGTGTGCCAAAGGGAGTGTCCATGGCAGGTCCTGTTG
 670 680 690 700 710 720

+180 +190
 Leu Val Asn Gly Ala Gln Leu Cys Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser
 TTGGTGAATGGAGCTCAGTTGTGGGGGACCTGATCAACACCATCTGGTGCTCTCC
 730 740 750 760 770 780

+200 +210
 Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu
 GCGGCCACTGTTCGACAAAATCAAGAACCTGGAGAACCTGATCGCGTGCTGGCAGG
 790 880 810 820 830 840

+220 +230
 His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile
 CACGACCTCAGCGAGCACGACGGGATGAGCAGAGCCGGCGGGTGGCGCAGGTCATCATC
 850 860 870 880 890 900

+240 +250
 Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 CCCAGCACGTACGTCCCAGGACCACCAACCACGACATCGCGCTGCTCCGCCTGCACCA
 910 920 930 940 950 960

+260 +270
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu
 CCCGTGGTCTCACTGACCATGTGGTGGCCCTCTGCCTGCCAACGGACGTTCTCTGAG
 970 980 990 1000 1010 1020

+280 +290
 Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg
 AGGACGCTGGCCTCTCGTGGCTCTCATGGTCAGCGGCTGGGCCAGCTGCTGGACCGT
 1030 1040 1050 1060 1070 1080

+300 +310
 Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys
 GGCCCCACGGCCTGGAGCTCATGGCTCAACGTGCCCGCTGATGACCCAGGACTGC
 1090 1100 1110 1120 1130 1140

+320 +330
 Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 CTGCACTGGATGGCAGCAAGGACTCCTGCAAGGGGGACAGTGAGGCCACATGTTCTGTGCC
 1150 1160 1170 1180 1190 1200

+340 +350
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr
 GGCTACTCGGATGGCAGCAAGGACTCCTGCAAGGGGGACAGTGAGGCCACATGCCACC
 1210 1220 1230 1240 1250 1260

+360 +370
 His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr
 CACTACCGGGCACGTGGTACCTGACGGGCATCGCAGCTGGGCCAGGGCTGCGCAACC
 1270 1280 1290 1300 1310 1320

+380 +390
 ValGlyHisPheGlyValTyrThrArgValSerGlnTyrIleGluTrpLeuGlnLysLeu
 GTGGCCCACTTGGGGTGTACACCAAGGGCTCCCAGTACATCGACTGGCTGC
 1330 1340 1350 1360 1370 1380

+400 +406
 Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro ***
 ATGC GCT CAG AGC CAC GCC AGG AGT CCT CTC GAG CCC ATT TCC CTA G
 1390 1400 1410 1420 1430 1440

CCTGGCCTGTGGAGAGAAAGCCAAGGCTGCGT CGAAC TGT CCTGGCACCAAT C
 1450 1460 1470 1480 1490 1500

ATTCTTCTGCAGTTAATGGGGTAGAGGAGGGCATGGGAGGGAGGGAGGGTGGGGAGGG
 1510 1520 1530 1540 1550 1560

GACAGAGACAGAAACAGAGAGAGACAGAGACAGAGAGACTGAGGGAGAGACTCTGAGG
 1570 1580 1590 1600 1610 1620

ACATGGAGAGAGACTCAAAGAGACTCCAAGATTCAAAGAGACTAATAGAGACACAGAGAT
 1630 1640 1650 1660 1670 1680

GGAA TAG AAA AGATGAGAGG CAGAGG CAGACGG C GCTGG ACAGAGGG CAGGGG AGTGC
 1690 1700 1710 1720 1730 1740

CAAGGTTGTCTGGAGGCAGACAGCCCAGCTGAGCCTCTTACCTCCCTTCAGCCAAGCC
 1750 1760 1770 1780 1790 1800

CCACCTGCACGTGATCTGCTGGCCCTCAGGCTGCTGCTCTGCCTTCATTGCTGGAGACAG
 1810 1820 1830 1840 1850 1860

TAGAGGCATGAACACACATGGATGCACACACACACACGCCAATGCACACACACAGAGATA
 1870 1880 1890 1900 1910 1920

TGCACACACAGGATGCACACACAGATGGTACACAGAGATA TGCACACACACCAGATGC
 1930 1940 1950 1960 1970 1980

CACGCACATAGAGATATGCACACACAGATGCACACACAGATATACATGGATGCACGCA
 1990 2000 2010 2020 2030 2040

CATGCCAATGCACGCACACATCA GTGCACACGGATGCACAGAGATATGCACACACCGATG
 2050 2060 2070 2080 2090 2100

TGGCCACACACAGATATGCACACACATGGATGAGCACACACACACCAAGTGCGCACACAC
 2110 2120 2130 2140 2150 2160

ACCGATGTACACACACAGATGCACACACAGATGCACACACACCCGATGCTGACTCCATGTG
 2170 2180 2190 2200 2210 2220

TGCTGTCTCTGAAGGGCGTTGTTAGCTCTCAC TTTCTGGTTCTATCCATTATCATC
 2230 2240 2250 2260 2270 2280

TTCACCTTCAGACAATTCAAGGCATCACCATGCATGGTGGCGAATGCCCCAAA CTCC
 2290 2300 2310 2320 2330 2340

CCCCAATGTATTCCTCCCTCGCTGGGTGCCGGGCTGCACAGACTATTCCCCACCTGCTT
 2350 2360 2370 2380 2390 2400

CCCAGCTTCACAATAAACGGCTGCCTCTCCTCCGCACACCTGTGGTGCCTGCCACCCAAA
2410 2420 2430 2240 2450 2460

AAAAAAAAAAAAAA
2470 2480

	1	10	20	30	40
FACTOR VII	AN A - FLY Y L R P G S L Y Q C S F Y Y A R Y F Y X X X R T K L		*	*	*
FACTOR IX	Y N S G K L Y Y F V Q G N L Y R Y C H M Y Y K C S F Y Y A R Y F Y N T Y R T Y		*	*	*
FACTOR X	A N S - F L Y Y M K K G H L Y R Y C H M Y Y T C S Y Y Y A R Y F Y D S D K T N Y		*	*	*
PROTEIN C	A N S - F L Y Y R H S S L Y R Y C I Y Y I C D F Y Y A Y L Y I F Q N V D D T L A		*	*	*
PROTHROMBIN	A N T - F L Y Y V R K G N L Y R Y C V Y Y T C S Y Y Y A F Y A L Y S T A T D V		*	*	*

FIG.^o
2A

	50	60	70
FACTOR VII	F W I S Y S D G D Q C A S S - - - -	- - - - P C Q N G G S C K D D Q L Q S T I C P	
FACTOR IX	F W K Q Y V D G D Q C E S N - - - -	- - - - P C P L N G G S C K B D I N S T E C W	
FACTOR X	F W N K Y K D G D Q C E T S - - - -	- - - - P C Q N Q G K C K B G L G E Y T C T	
PROTEIN C	F W S K H V D G D Q C L V L P L E R P C A S L C C G H G T C I B G I G S F S C D		
PROTHROMBIN	F W A K Y T A C E T A R T P R D K L A A C L E G N C A E G L C T N Y R G H V N I		

	80	90	100	110
FACTOR VII	C L P A F E G R N C E T H K D D Q L I C V N E N G C E Q Y I C S D H T G I K R S C			
FACTOR IX	C P F G F E G K N C E L D V T - - - C N I K N G R C E Q F C K N S A D N K V V C			
FACTOR X	C L E G F E G K N C E L F T R K L - - - C S L D N G D C D Q F C H E E Q N S - V V C			
PROTEIN C	C R S G W E G R F C Q R E V S F L N - C S L D N G G C T H Y C L E E V G W - R R C			
PROTHROMBIN	T R S G I E C Q L W R S K R Y P H K P - E I N S T T H P C A D L Q E N Y C R N P D S			

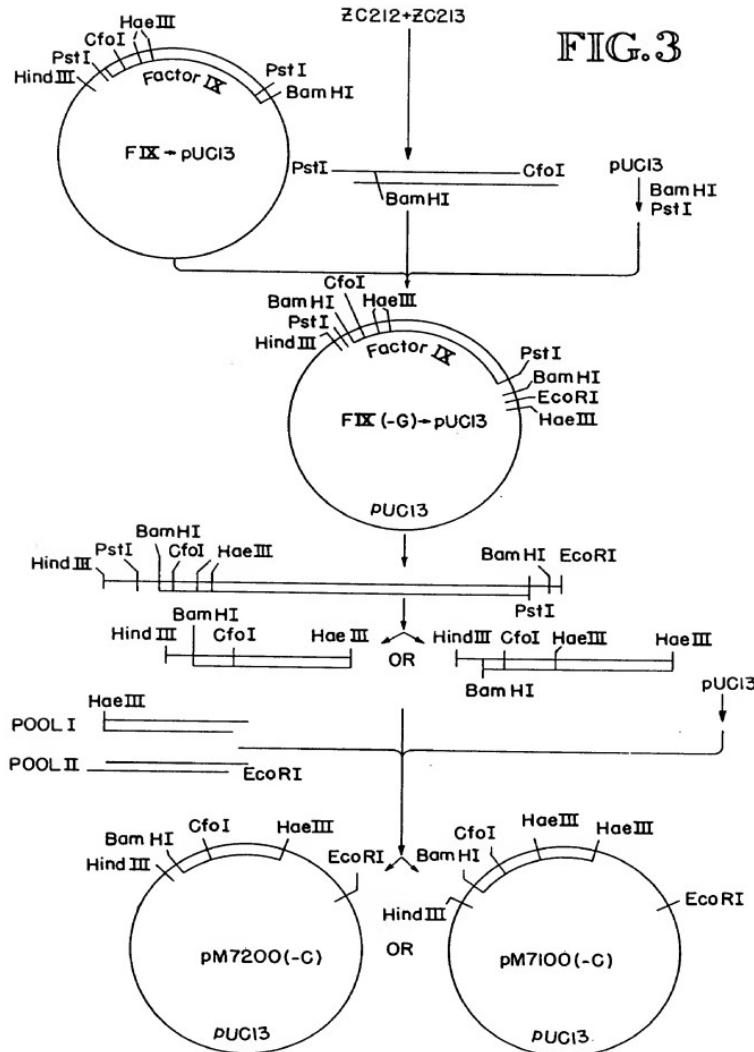
FACTOR VII	R C H E G Y S L L A D G V S C T P T V E Y P C G K I P I L E K R N A S K P Q G R
FACTOR IX	S C T E G Y R L A G N Q K S C E P A V P F F P C G R V S V S Q T S K L R T
FACTOR X	S C A R G Y T L A D N G K A C I P T G P Y P C C G K Q T L E R
PROTEIN C	S C A P G Y K L G C D D L L Q C H P A V K F P C G R P W K R M E K K R S H L
PROTHROMBIN	S N T G P W C Y T T D P T V R R Q E C S I P V U C G Q D Q V T V A M T P R S

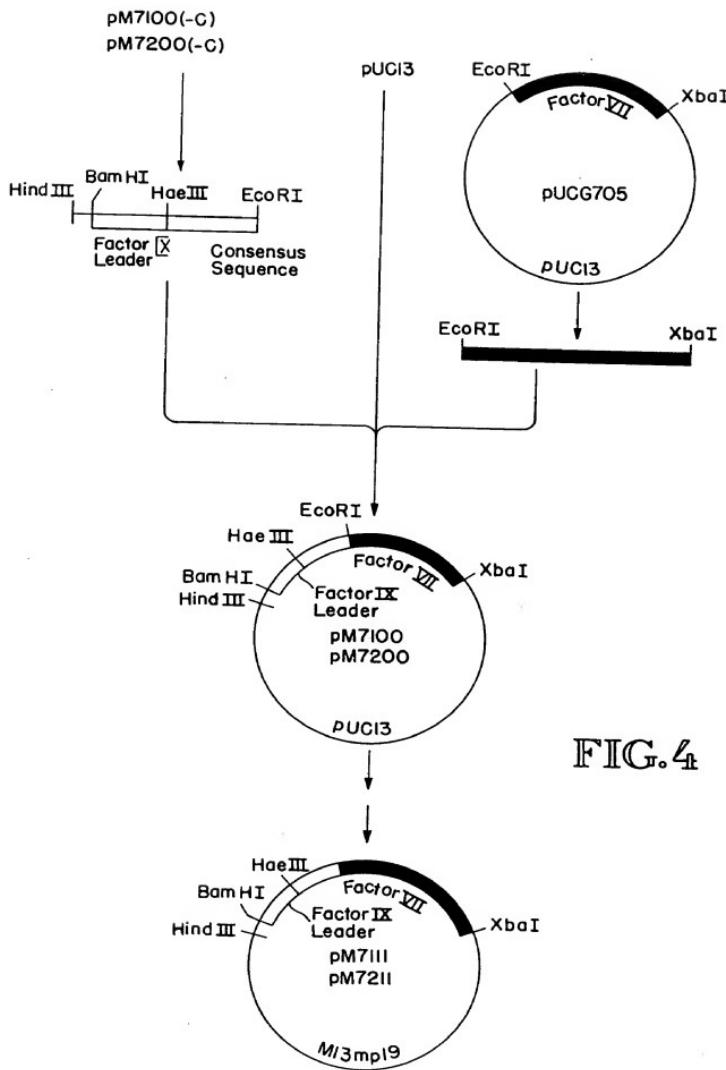
FIG.
2B

	40	50	60	70
cDNA	KLFWISYSDG DQCASSP CQNGS CKD QLQ S YIC F CL	LFWISYSDG DQCASSP CQNGS CKD QLQ		
Amino Acid Sequence	P A F E G R N C E T R K D D D Q L I C V N E N G C E Q Y C S D R T G T K	P A F E G R N C E T H K D D Q L		

Amino Acid Sequence	cDNA
110	R S C R C H E G Y S L L A D G V S C T P T V E Y P C G K I P I L E K R N
120	S C R C H E G Y S L L A D G V S C T P T V E Y
130	
140	E K R (

FIG. 3





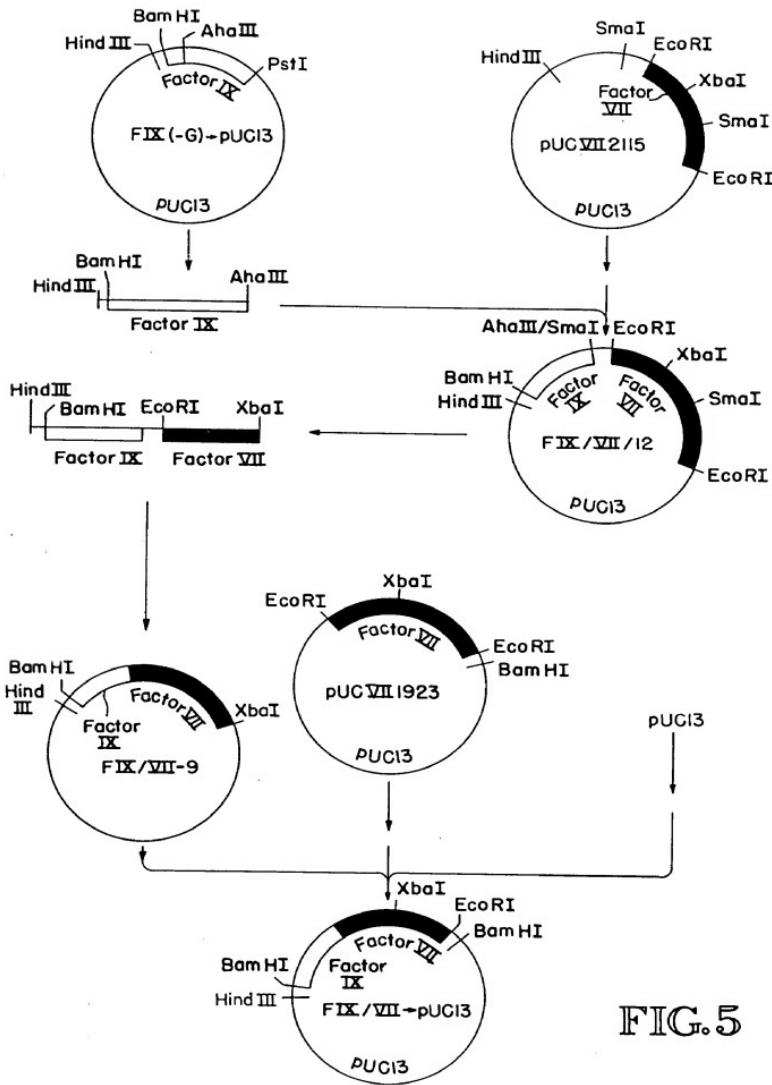


FIG. 5

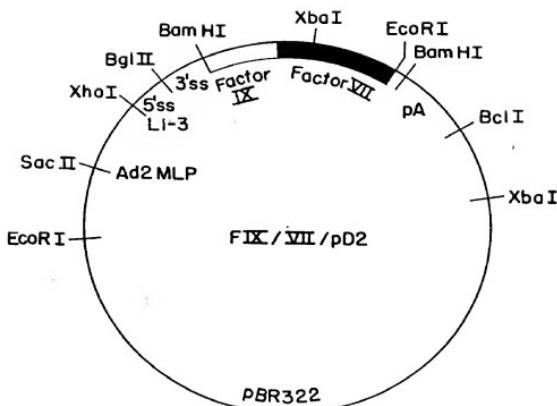


FIG. 6

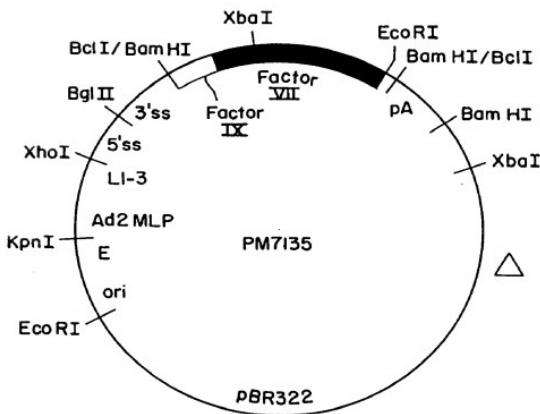


FIG. 8

FIG. 7

GGATCC ATG CAG CGC GPG AAC ATG ATC ATG GCA GAA TCA CCA GGC MET Gln Arg Val Asn MET Ile MET Ala Glu Ser Pro Gly	21	36	
CTC ATC ACC ATC TGC CTT TTA GGA TAT CTA CTC AGT GCT GAA TGT Leu Ile Thr Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys	66	81	
ACA GTT TTT CTT GAT CAT GAA AAC GCC AAC AAA ATT CTG AAT CGG Thr Val Phe Leu Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg	96	111	126
CCA AAG AGG TAT AAT TCA GGT AAA TTG GAA GAG TTT GTT CAA GGG Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Phe Val Gln Gly	141	156	171
AAC CTT GAG AGA GAA TGT ATG GAA GAA AAG TGT AGT TTT GAA GAA Asn Leu Glu Arg Glu Cys MET Glu Glu Lys Cys Ser Phe Glu Glu	186	201	216
GCA CGA GAA GTT TTT GAA AAC ACT GAA AGA ACA AAG CTG TTC TGG Ala Arg Glu Val Phe Glu Asn Thr Glu Arg Thr Lys Leu Phe Trp	231	246	261
ATT TCT TAC AGT GAT GGG GAC CAG TGT GCC TCA AGT CCA TGC CAG Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln	276	291	306
AAT GGG GGC TCC TGC AAG GAC CAG CTC CAG TCC TAT ATC TGC TTC Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe	321	336	351
TGC CTC CCT GCC TTC GAG GGC CGG AAC TGT GAG ACG CAC AAG GAT Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp	366	381	396
GAC CAG CTG ATC TGT GTG AAC GAG AAC GGC GGC TGT GAG CAG TAC Asp Glu Leu Ile Cys Val Asn Glu Asn Gly Cys Glu Gln Tyr	411	426	441
TGC AGT GAC CAC ACG GGC ACC AAG CGC TCC TGT CGG TGC CAC GAG Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu	456	471	486
GGG TAC TCT CTG CTG GCA GAC GGG GTG TCC TGC ACA CCC ACA GTT Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val	501	516	531
GAA TAT CCA TCT GGA AAA ATA CCT ATT CTA GAA AAA AGA AAT GCC Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala	546	561	576
AGC AAA CCC CAA GGC CGA ATT GTG GGG GGC AAG GTG TGC CCC AAA Ser Lys Pro Gln Gly Arg Ile Val Gly Lys Val Cys Pro Lys	591	606	621

636	651	666
GGG GAG TGT CCA TGG CAG GTC CTG TTG GTG AAT	GGA GCT CAG	
Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln		
681	696	711
TTG TGT GGG GGG ACC CTG ATC AAC ACC ATC TGG GTG GTC TCC GCG		
Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala		
726	741	756
GCC CAC TGT TTC GAC AAA ATC AAG AAC TGG AGG AAC CTG ATC GCG		
Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala		
771	786	801
GTG CTG GGC GAG CAC GAC CTC AGC GAG CAC GAC GGG GAT GAG CAG		
Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln		
816	831	846
AGC CGG CGG GTG GCG CAG GTC ATC ATC CCC AGC ACG TAC GTC CCG		
Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro		
861	876	891
GGC ACC ACC AAC CAC GAC ATC GCG CTG CTC CGC CTG CAC CAG CCC		
Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln Pro		
906	921	936
GTG GTC CTC ACT GAC CAT GTG GTG CCC CTC TGC CTG CCC GAA CGG		
Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg		
951	966	981
ACG TTC TCT GAG AGG ACG CTG GCC TTC GTG CGC TTC TCA TTG GTC		
Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val		
996	1011	1026
AGC GGC TGG GGC CAG CTG CTG GAC CGT GGC GCC ACG GCC CTG GAG		
Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu		
1041	1056	1071
CTC ATG GTC CTC AAC GTG CCC CGG CTG ATG ACC CAG GAC TGC CTG		
Leu MET Val Leu Asn Val Pro Arg Leu MET Thr Gln Asp Cys Leu		
1086	1101	1116
CAG CAG TCA CGG AAG GTG GGA GAC TCC CCA AAT ATC ACG GAG TAC		
Gln Gln Ser Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr		
1131	1146	1161
ATG TTC TGT GCC GGC TAC TCG GAT GGC AGC AAG GAC TCC TGC AAG		
MET Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys		
1176	1191	1206
GGG GAC AGT GGA GGC CCA CAT GCC ACC CAC TAC CGG GGC ACG TGG		
Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr Trp		
1221	1236	1251
TAC CTG ACG GGC ATC GTC AGC TGG GGC CAG GGC TGC GCA ACC GTG		
Tyr Leu Thr gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val		

1266 1281 1296
GGC CAC TTT GGG GTG TAC ACC AGG GTC TCC CAG TAC ATC GAG TGG
Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp

1311 1326 1341
CTG CAA AAG CTC ATG CGC TCA GAG CCA CGC CCA GGA GTC CTC CTG
Leu Gln Lys Leu MET Arg Ser Glu Pro Arg Pro Gly Val Leu Leu

1356 1378 1388 1398
CGA GCC CCA TTT CCC TAG CCCAGCAGCC CTGGCCTGTG GAGAGAAAGC
Arg Ala Pro Phe Pro

1408 1418 1428 1438 1448
CAAGGCTGCG TCGAACTGTC CTGGCACCAA ATCCCATATA TTCTTCTGCA

1458 1468 1478 1488 1498
GTTAACGGGG TAGAGGAGGG CATGGGAGGG AGGGAGAGGT GGGGAGGGAG

1508 1518 1528 1538 1548
ACAGAGACAG AAACAGAGAG AGACAGAGAC AGAGAGAGAC TGAGGGAGAG

1558 1568 1578 1588 1598
ACTCTGAGGA CCATGGAGAG AGACTCAAAG AGACTCCAAG ATTCAAAGAG

1608 1618 1628 1638 1648
ACTAAATAGAG ACACAGAGAT GGAATAGAAA AGATGAGAGG CAGAGGCAGA

1658 1668 1678 1688 1698
CAGGGCCTGAG ACAGAGGGGC AGGGGAGTGC CAAGGTTGTC CTGGAGGCAG

1708 1718 1728 1738 1748
ACAGCCCAGC TGAGCCTCCT TACCTCCCTT CAGCCAAGCC CCACCTGCAC

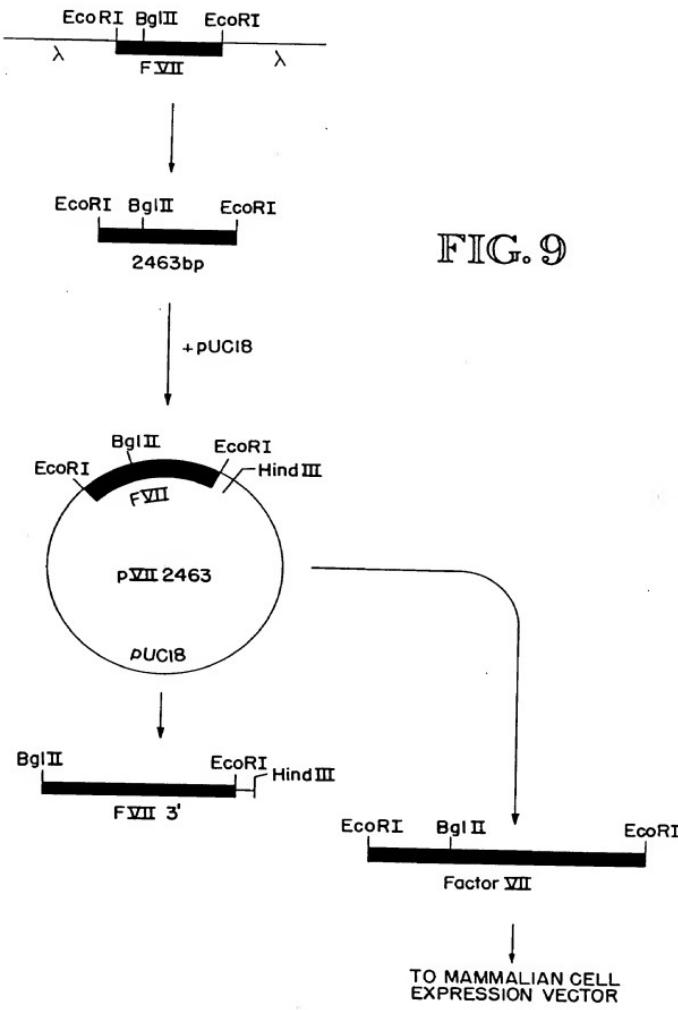
1758 1768 1778 1788 1798
GTGATCTGCT GCCCCTCAGG CTGCTGCTCT GCCTTCATTG CTGGAGACAG

1808 1818 1828 1838 1848
TAGAGGCATG ACACACATGG ATGCACACAC ACACACGCCA TGCACACACA

1858 1868 1878 1888 1898
CAGAGATATG CACACACACG GATGCACACACA CAGATGGICA CACAGAGTAC

1908 1918 1928 1938 1948
GCAAACACAC CGATGACAC GCACATAGA ATATGCACAC ACAGATGCAC

1958	1968	1978	1988	1998
ACACAGATAT	ACACATGGAG	TGCACGCACA	TGCCAATGCA	CGCACACATC
2008	2018	2028	2038	2048
AGTGCACACG	GATGCACAGA	GATATGCACA	CACCGATGTG	CGCACACACAA
2058	2068	2078	2088	2098
GATATGCACA	CACATGGATG	AGCACACACAA	CACCAAGTGC	GCACACACAC
2108	2118	2128	2138	2148
CGATGTACAC	ACAGATGCAC	ACACAGATGC	ACACACACCG	ATGCTGACTC
2158	2168	2178	2188	2198
CATGTGTGCT	GTCCTCTGAA	GGCGGTTGTT	TAGCTCTCAC	TTTCTGGTT
2208	2218	2228	2238	2248
CTTATCCATT	ATCATCTTCA	CTTCAGACAA	TTCAGAAGCA	TCACCATGCA
2258	2268	2278	2288	2298
TGGTGGCGAA	TGCCCCAAA	CTCTCCCCA	AATGTATTTC	TCCCTTCGC1
2308	2318	2328	2338	2348
GGGTGCCGGG	CTGCACAGAC	TATTCCCCAC	CTGCTTCCC	GCTTCACAAT
2358	2368	2378	2388	2398
AAACGGCTGC	GTCTCCTCGC	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA
2408	2418	2428	2438	
AAAAAAAAAA	AAGGAATTG	AGCTCGGTAC	CCGGGGATCC	



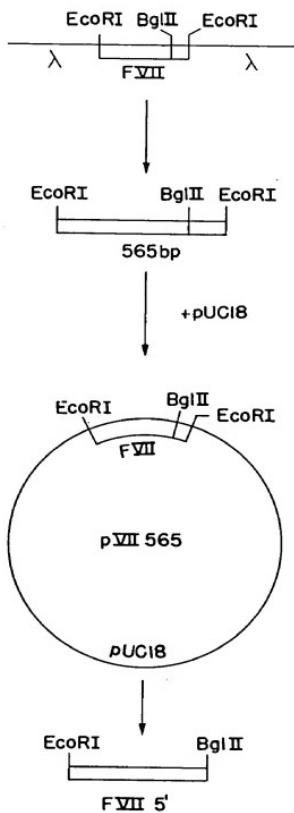


FIG. 10

FIG. II

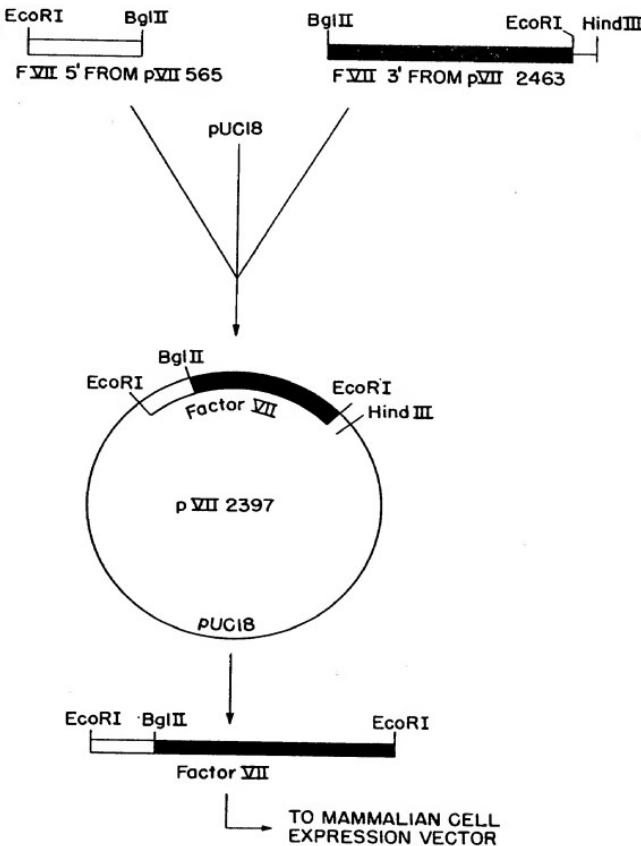


FIG. 12

